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[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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General information about the entry

Entry name	**Q9SY11**
Primary accession number	**Q9SY11**
Secondary accession numbers	None
Entered in TrEMBL in	Release 13, May 2000
Sequence was last modified in	Release 13, May 2000
Annotations were last modified in	Release 24, June 2003

Name and origin of the protein

Protein name	**Similar to PHZF, CATALYZING the HYDROXYLATION of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid**
Synonyms	None
Gene name	**T5J8.18 or AT4G02860**
From	Arabidopsis thaliana (Mouse-ear cress) [TaxID: 3702]
Taxonomy	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=cv. Columbia;
de la Bastide M., Gnoj L., Habermann K., Huang E.N., Gottesman T., Kaplan N., Lodhi M., Jensen K., Hameed A., Schutz K., Martienssen R., Dedhia N., Parnell L.D., McCombie W.R.;
"Arabidosis thaliana BAC T5J8 from chromosome IV, short arm.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

[2] SEQUENCE FROM NUCLEIC ACID.
Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

[3] SEQUENCE FROM NUCLEIC ACID.
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

Comments

None

Cross-references

EMBL	AC004044; AAD15343.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AL161495; CAB77771.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
GO	GO:0003824; Molecular function: enzyme activity *(inferred from electronic annotation)*. GO:0009058; Biological process: biosynthesis *(inferred from electronic annotation)*.
TAIR	Q9SY11; AT4G02860.
InterPro	IPR003719; PhzC_PhzF. Graphical view of domain structure.
Pfam	PF02567; PhzC-PhzF; 1.
TIGRFAMs	TIGR00654; PhzF_family; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
ProtoMap	Q9SY11.
PRESAGE	Q9SY11.
ModBase	Q9SY11.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Hypothetical protein.

Features

None

Sequence information

Length: **294 AA**	Molecular weight: **32085 Da**	CRC64: **73E27F7AE184F0A2** [This is a checksum on the sequence]

```
          10          20          30          40          50          60
           |           |           |           |           |           |
MGKKKGVKYF VVDAFTDSAF KGNPAAVCFL NDDNERDDTW LQSLAAEFNI SETCFLIPIT

          70          80          90         100         110         120
           |           |           |           |           |           |
GFQARFSLRW FTPLAEVDLC GHATLASAHC LFSNGLVDSD MVEFVTRSGI LTAKRVSDTS

         130         140         150         160         170         180
           |           |           |           |           |           |
ELSDGEVKGG TFLIELNFPV VTTCDVNLSD VSSSMITKAL NGATIVDIKA TATNNILVVL

         190         200         210         220         230         240
           |           |           |           |           |           |
PSKESVTELQ PRMDDILKCP CDGIIVTAAG STGSSYDFYS RYFAPKFGVD EDPVCGSAHC

         250         260         270         280         290
           |           |           |           |           |
ALAHYWSIKM NKFDFLAYQA SSRSGTIRIH LDKEKQRVLL RGKAVTVMEG HVLV
```

Q9SY11 in FASTA format

View entry in original TrEMBL format
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BLAST   **BLAST submission on ExPASy/SIB or at NCBI (USA)**

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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